

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 18, 2002, 10:14:33 ; Search time 211.29 Seconds
(without alignments)
73.036 Million cell updates/sec

Title: US-09-651-846-1

Perfect score: 18

Sequence: 1 gacgcgtggtggccccat 18

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match: 0%

Maximum Match: 100%
Listing first 45 summaries

Database :

1: N_Geneseq_1101: *
2: /SID2/gcgcdata/geneseq/geneseqn/NA1980.DAT: *
3: /SID2/gcgcdata/geneseq/geneseqn/NA1981.DAT: *
4: /SID2/gcgcdata/geneseq/geneseqn/NA1982.DAT: *
5: /SID2/gcgcdata/geneseq/geneseqn/NA1983.DAT: *
6: /SID2/gcgcdata/geneseq/geneseqn/NA1984.DAT: *
7: /SID2/gcgcdata/geneseq/geneseqn/NA1985.DAT: *
8: /SID2/gcgcdata/geneseq/geneseqn/NA1986.DAT: *
9: /SID2/gcgcdata/geneseq/geneseqn/NA1987.DAT: *
10: /SID2/gcgcdata/geneseq/geneseqn/NA1988.DAT: *
11: /SID2/gcgcdata/geneseq/geneseqn/NA1989.DAT: *
12: /SID2/gcgcdata/geneseq/geneseqn/NA1990.DAT: *
13: /SID2/gcgcdata/geneseq/geneseqn/NA1991.DAT: *
14: /SID2/gcgcdata/geneseq/geneseqn/NA1992.DAT: *
15: /SID2/gcgcdata/geneseq/geneseqn/NA1993.DAT: *
16: /SID2/gcgcdata/geneseq/geneseqn/NA1994.DAT: *
17: /SID2/gcgcdata/geneseq/geneseqn/NA1995.DAT: *
18: /SID2/gcgcdata/geneseq/geneseqn/NA1996.DAT: *
19: /SID2/gcgcdata/geneseq/geneseqn/NA1997.DAT: *
20: /SID2/gcgcdata/geneseq/geneseqn/NA1998.DAT: *
21: /SID2/gcgcdata/geneseq/geneseqn/NA1999.DAT: *
22: /SID2/gcgcdata/geneseq/geneseqn/NA2000.DAT: *
23: /SID2/gcgcdata/geneseq/geneseqn/NA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	35	20	AA36573
C 2	18	100.0	35	22	AA500262
C 3	13.2	73.3	19	18	AA796666
C 4	13.2	73.3	19	21	AA94661
C 5	13.2	73.3	30	20	AA225676
C 6	13.2	73.3	30	20	AA225680
C 7	13.2	73.3	48	21	AA446997
C 8	12.8	71.1	31	21	AA258151
C 9	12.8	71.1	33	20	AA559895
C 10	12.8	71.1	33	20	AA559894
C 11	12.4	68.9	27	20	AA80155

ALIGNMENTS

12	12.4	68.9	27	21	AA53308	PCR primer hGT-6SP
13	12.4	67.8	36	17	AA737043	Tobacco mosaic vir
14	12.2	67.8	17	20	AAV93456	Human B-raf subutr
15	12.2	67.8	20	17	AA712422	Antiviral phosphor
16	12.2	67.8	20	17	AA712426	Antiviral phosphor
17	12.2	67.8	20	17	AA712430	Antiviral phosphor
18	12.2	67.8	20	17	AA712431	Antiviral phosphor
19	12.2	67.8	20	17	AA712436	Antiviral phosphor
20	12.2	67.8	36	22	AA724433	Antiviral phosphor
21	12.2	67.8	36	22	AA724434	T reesel cellbioh
22	12.2	67.8	51	22	AAH89385	T reesel cellbioh
23	11.8	65.6	16	17	AA712432	Human structural p
24	11.8	65.6	19	20	AA225440	Antiviral phosphor
25	11.8	65.6	21	22	AA724436	Human PD2 antisens
26	11.8	65.6	20	17	AA712429	Antiviral phosphor
27	11.8	65.6	21	18	AA796380	Antiviral phosphor
28	11.8	65.6	21	18	AA776851	Hepatitis GB virus
29	11.8	65.6	21	22	AA776435	Primer for HGBV NT
30	11.8	65.6	21	22	AA776436	Codon-optimised HP
31	11.8	65.6	25	15	AAO54748	Codon-optimised HP
32	11.8	65.6	27	19	AAV60330	Epstein-Barr virus
33	11.8	65.6	28	21	AAA40094	PCR primer R0097 u
34	11.8	65.6	29	18	AA785072	Human lysophosphat
35	11.8	65.6	32	22	AAH25021	Bacteriophage m13m
36	11.8	65.6	35	19	AAV00372	PCR primer used to
37	11.8	65.6	35	22	AA773290	Bacillus thuringie
38	11.8	65.6	36	22	AA794659	Oligonucleotide #8
39	11.8	65.6	36	22	AA729275	C12-9 PCR primer f
40	11.8	65.6	38	21	AAZ34639	Primer for CDNA en
41	11.8	65.6	39	14	AAQ37427	Granulocyte colony
42	11.8	65.6	45	17	AA715672	Primer -21MO10BKE
43	11.8	65.6	45	17	AA708869	Reverse-Frame HGV
44	11.8	65.6	45	19	AAV66128	Primer GE-3F for H
45	11.8	65.6	45	19	AAV56087	PCR primer GE-3F u
					AAV22787	HGV primer GE-3F D
						Capture/amplificat

RESULT 1	AA36573/c	AA36573 standard; DNA; 35 BP.
ID	AA36573	
AC	AA36573	
XX		
DT	07-JUL-1999	(first entry)
XX		
DE	PCR primer for human EDG-1 coding sequence.	
XX		
KW	EDG-1; EDG-2; EDG-3; EDG-4; EDG-5; PSP-24; human; detection; therapy;	
KW	inverse agonist; allosteric modulator; lysophosphatidic acid receptor;	
KW	LPA signalling mediated disease; cellular apoptosis; PCR primer; ss.	
XX		
OS	Synthetic.	
OS	Home-septins	
XX		
PN	WO9919513-A2	
XX		
PD	22-APR-1999	
XX		
PF	09-OCT-1998	98WO-US21315.
XX		
PR	10-OCT-1997	97US-0061572.
XX		
PA	(LXRB-) LXR BIOTECHNOLOGY INC.	
XX		
PI	Erikson J, Goddard JG, Kiefer M.	
XX		
DR	WPI: 1999-277658/23.	
XX		
PT	Identification of (ant)agonists of LPA receptor EDG-2 for, e.g.	
XX	treating LPA signalling mediated diseases such as cellular apoptosis	

PS Example 1; Page 30; 63pp; English.

CC This sequence is a PCR primer for DNA encoding human EDG-1.
 CC The invention relates to methods of detecting (ant)agonist, inverse
 CC agonist or allosteric modulators of the lysophosphatidic acid receptors
 CC EDG-1, EDG-2, EDG-3, EDG-4, EDG-5, and PSP-24. The methods are used to
 CC identify (ant)agonists and allosteric modulator of the lysophosphatidic
 CC acid (LPA) EDG2 receptor, e.g. to treat LPA signalling mediated disease
 CC such as cellular apoptosis.

Sequence 35 BP; 5 A; 15 C; 12 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 35;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gacgtgtgtggcccat 18
 DB 32 GACGCTGTGGCCCAT 15

RESULT 2

AAS0262/C
 ID AAS00262 standard; DNA; 35 BP.

AC AAS00262;

DE -11-MAY-2001 (first entry)

XX LPA receptor-related primer #1.

KW LPA receptor; EDG-2; lysophosphatidic acid; phospholipid; tumour;
 KW cell signalling; MAP kinase; LPA modulator; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuron damage; apoptosis;
 KW ischaemic heart disease; viral; HIV; inflammatory bowel disease;
 KW organ transplant; ss.

OS Unidentified.

PN WO200112838-A2.

PD 22-FEB-2001.

PF 11-AUG-2000; 2000WO-US22101.

PR 18-AUG-1999; 99US-0376399.

PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.

PI Erickson J, Goddard JG, Kiefer M, Picker D;

DR WPI; 2001-226550/23.

XX Modulating activity of a lysophosphatidic acid or its receptor for
 PT treating tumours, viral diseases, involves introducing to LPA or its
 PT receptor a composition containing diol, epoxide or phosphate compound
 PT
 XX Disclosure; Page 87; 89pp; English.

CC The sequence represents the LPA receptor-related primer #1 used during
 CC analysis of lysophosphatidic acid receptor (LPA), EDG-2. The sequence is
 CC given in the specification but no further information is given. LPA is a
 CC phospholipid found in a variety of plant and animal products. EDG-2 is
 CC involved in cell signalling through activation of a MAP kinase cascade
 CC dependent receptor. Modulating the activity of a lysophosphatidic acid
 CC (LPA) or LPA receptor (EDG-2) involves introducing a composition
 CC comprising LPA modulators to the LPA or receptor. The method is useful
 CC for treating diseases characterised by slowed growth or repair of
 CC neuronal cells, neurodegenerative diseases, such as Alzheimer's disease,
 CC Parkinson's disease, and acute neuron damage, for modulating apoptotic
 CC pathways and treating ischaemic heart disease, tumours, viral diseases

CC bowel disease, and rejection of organ transplants.

XX Sequence 35 BP; 5 A; 15 C; 12 G; 3 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gacgtgtgtggcccat 18
 DB 32 GACGCTGTGGCCCAT 15

RESULT 3

AAT96666/C
 ID AAT96666 standard; cDNA; 19 BP.

AC AAT96666;

DE 27-APR-1998 (first entry)

XX Human TUB gene 3' end primer for radiation hybrid mapping.

KW TULP; tub gene; human; sensory neuron; neurosensory defect;
 KW cochlear degeneration; hearing loss; deafness; retinal dystrophy;
 KW retinitis pigmentosa; combined rod cone dystrophy; obesity;
 KW animal model; transgenic animal; therapy; diagnosis; PCR; primer;
 KW ss.

OS Synthetic.

OS Homo sapiens.

PN WO9738004-A1.

PD 16-OCT-1997.

PF 10-APR-1997; 97WO-US05903.

PR 17-SEP-1996; 96US-0714991.

PR 10-APR-1996; 96US-0630592.

PR 22-AUG-1996; 96US-0701380.

PR 04-SEP-1996; 96US-0706292.

PA (JACK-) JACKSON LAB.

PA (SEOU-) SEQUANA THERAPEUTICS INC.

PI Neggert J, Nishina P, Noben-Trauth K, North M;

DR WPI; 1997-512642/47.

XX Mammalian TULP protein - used for detecting pre-disposition to
 PT neuro-sensory defects
 PT
 XX Disclosure; Page 35; 89pp; English.

CC PCR primers (AAT96663 and AAT96664) were designed for the 3' non-coding
 CC region of the human TUB gene (see AAT96639) and were used in
 CC radiation hybrid mapping, generating a product of 221 bp. Another
 CC primer pair (see AAT96661-62) amplified the 5' region of TUB, and a
 CC further pair (see AAT96665-66) amplified TULP cDNA (see AAT96642).
 CC TUB and TULP are novel members of the mammalian TULP gene family
 CC associated with various defects in sensory neurons such as
 CC cochlear defects, retinitis pigmentosa and combined rod-cone
 CC dystrophy.

Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 other;

Query Match 73.3%; Score 13.2; DB 18; Length 19;
 Best Local Similarity 83.3%; Pred. No. 2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

PS Example 1; Page 30; 63pp; English.
 CC This sequence is a PCR primer for DNA encoding human EDG-1.
 CC The invention relates to methods of detecting (ant)agonist, inverse
 CC agonist or allosteric modulators of the lysophosphatidic acid receptors
 CC EDG-1, EDG-2, EDG-3, EDG-4, EDG-5, and PGP-24. The methods are used to
 CC identify (ant)agonists and allosteric modulator of the lysophosphatidic
 CC acid (LPA) EDG2 receptor, e.g. to treat LPA signalling mediated disease
 CC such cellular apoptosis.
 CC
 CC Sequence 35 BP; 5 A; 15 C; 12 G; 3 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 20; Length 35;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggtgagcccatggt 18
 |||
 DB 29 GCTGTTGGCCCATGTT 12

RESULT 2
 AAS00262/C
 ID AAS00262 standard; DNA; 35 BP.
 XX
 AC AAS00262;
 XX
 DT -11-MAY-2001 (first entry)
 XX
 DE LPA receptor-related primer #1.
 XX
 KW LPA receptor; EDG-2; lysophosphatidic acid; phospholipid; tumour;
 KW cell signalling; MAP kinase; LPA modulator; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; neuron damage; apoptosis;
 KW ischaemic heart disease; viral; HIV; inflammatory bowel disease;
 KW organ transplant; ss.
 XX
 OS Unidentified.
 XX
 PN WO200112838-A2.
 PD
 XX 22-FEB-2001.
 XX
 PF 11-AUG-2000; 2000WO-US-101.
 XX
 PR 18-AUG-1999; 99US-037499.
 XX
 PA (ATAI-) AFAIRGIN TECHNOLOGIES INC.
 PI Erickson J, Goddard JG, Kiefer M, Pickler D;
 DR WPI: 2001-226550/23.
 XX
 PT Modulating activity of a lysophosphatidic acid or its receptor for
 PT treating tumours, viral diseases, involves introducing to LPA or its
 PT receptor a composition containing diol, epoxide or phosphate compound
 PT
 XX
 PS Disclosure: Page 87; 89pp; English.
 XX
 CC The sequence represents the LPA receptor-related primer #1 used during
 CC analysis of lysophosphatidic acid receptor (LPA), EDG-2. The sequence is
 CC given in the specification but no further information is given. LPA is a
 CC phospholipid found in a variety of plant and animal products. EDG-2 is
 CC involved in cell signalling through activation of a MAP kinase cascade-
 CC dependent reporter. Modulating the activity of a lysophosphatidic acid
 CC (LPA) or LPA receptor (EDG-2) involves introducing a composition
 CC comprising LPA modulators to the LPA or receptor. The method is useful
 CC for treating diseases characterised by slowed growth or repair of
 CC neuronal cells, neurodegenerative diseases, such as Alzheimer's disease,
 CC Parkinson's disease, and acute neuron damage, for modulating apoptotic
 CC pathways and treating ischaemic heart disease, tumours, viral diseases

CC bowel disease, and rejection of organ transplants.
 XX
 SQ Sequence 35 BP; 5 A; 15 C; 12 G; 3 T; 0 other;
 CC

Query Match 100.0%; Score 18; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctggtgagcccatggt 18
 |||
 DB 29 GCTGTTGGCCCATGTT 12

RESULT 3
 AAZ58151/C
 ID AAZ58151 standard; DNA; 31 BP.
 XX
 AC AAZ58151;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human FAST-1 gene PCR primer NT2-exp5'.
 XX
 KW FAST-1; hFAST-1; human; forkhead activin signal transducer;
 KW signal transduction; tumour-derived growth factor-beta; TGF-beta;
 KW activin; tumour; therapy; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200002910-A2.
 PD
 XX 20-JAN-2000.
 XX
 PF 18-JUN-1999; 99WO-US13764.
 XX
 PR 10-JUL-1998; 98US-0113309.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PI Zhou S, Zawal L, Vogelstein B, Kinzler KW;
 DR WPI: 2000-160897/14.
 XX
 PT Novel human forkhead activin signal transducer gene and polypeptides,
 PT used for screening for compounds which modulate the action of TGFbeta
 PT
 XX
 PS Example 6; Page 22; 47pp; English.
 XX
 CC The present sequence is that of primer NT2-exp5', which was used
 CC in the PCR amplification of human full-length FAST-1 (hFAST-1)
 CC open reading frame (see Z581440 using human colon CDNA as template.
 CC The PCR product was used in the construction of an expression
 CC vector that was utilised in experiments to demonstrate hFAST-1
 CC mediated transcriptional activation. hFAST-1 (see AAY58734) mediates
 CC transcriptional responses to tumour-derived growth factor-beta
 CC (TGF-beta) and activin in a ligand-, receptor- and smad-dependent
 CC fashion. The invention includes tools for investigating the
 CC TGF-beta signalling pathway and screening for compounds which
 CC modulate the action of TGF-beta. Such compounds can be used to
 CC modify or regulate transcriptional activation associated with the
 CC TGF-beta signalling pathway, and can be applied therapeutically to
 CC alter the growth of tumour cells, or to alter normal or abnormal
 CC developmental responses.
 CC
 CC Sequence 31 BP; 4 A; 12 C; 11 G; 4 T; 0 other;
 SQ

Query Match 82.2%; Score 14.8; DB 21; Length 31;
 Best Local Similarity 88.9%; Pred. No. 3 7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 18, 2002, 13:18:39 ; Search time 211.29 Seconds
(without alignments)
73.036 Million cell updates/sec

Title: US-09-651-846-2

Perfect score: 18
Sequence: 1 gctgtgtggcccatggt 18

Scoring table: IDENTITY_NGC
Gapop 10.0, Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101.*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	35	20	AA36573
C 2	18	100.0	35	22	AA500262
C 3	14.8	82.2	31	21	AA258151
C 4	13.8	76.7	27	20	AA80155
C 5	13.8	76.7	27	21	AA53308
C 6	13.4	74.4	31	19	AAV28442
C 7	13.2	73.3	45	19	AAV22787
C 8	13.2	73.3	45	19	AAV20737
C 9	13.2	73.3	48	21	AAA6997
C 10	12.8	71.1	21	18	AA796380
C 11	12.8	71.1	21	18	AA768851

C 12	12.8	71.1	22	21	AA01161
C 13	12.8	71.1	29	19	AA75543
C 14	12.8	71.1	30	20	AA225676
C 15	12.8	71.1	30	20	AA225680
C 16	12.8	71.1	33	21	AA668514
C 17	12.4	68.9	27	21	AA790893
C 18	12.4	68.9	31	18	AA768725
C 19	12.4	68.9	31	19	AAV45332
C 20	12.4	68.9	36	17	AA737043
C 21	12.4	68.9	37	21	AA294871
C 22	12.4	68.9	38	21	AA260175
C 23	12.2	67.8	20	21	AAA39285
C 24	12.2	67.8	20	21	AA231460
C 25	12.2	67.8	20	22	AA767593
C 26	12.2	67.8	20	22	AA91249
C 27	12.2	67.8	22	20	AA335965
C 28	12.2	67.8	22	22	AA508457
C 29	12.2	67.8	24	19	AAV13198
C 30	12.2	67.8	27	18	AA765526
C 31	12.2	67.8	27	18	AA762996
C 32	12.2	67.8	27	19	AAV5438
C 33	12.2	67.8	27	22	AA31126
C 34	12.2	67.8	28	14	AAQ34846
C 35	12.2	67.8	29	19	AAV42718
C 36	12.2	67.8	32	17	AA739712
C 37	12.2	67.8	32	18	AA779829
C 38	12.2	67.8	32	20	AA253321
C 39	12.2	67.8	32	20	AAV82882
C 40	12.2	67.8	33	17	AA739706
C 41	12.2	67.8	33	18	AA785136
C 42	12.2	67.8	33	18	AA779823
C 43	12.2	67.8	33	20	AA225315
C 44	12.2	67.8	33	20	AAV82876
C 45	12.2	67.8	34	21	AA54334

ALIGNMENTS

RESULT 1	AA36573/C	AA36573 standard; DNA; 35 BP.
ID	AA36573	
AC	AA36573	
XX		
DF	07-JUN-1999 (first entry)	
DE	PCR primer for human EDG-1 coding sequence.	
XX		
XX	EDG-1; EDG-2; EDG-3; EDG-4; EDG-5; PSP-24; human; detection; therapy;	
KW	Inverse agonist; allosteric modulator; lysophosphatidic acid receptor;	
KW	LPA signalling mediated disease; cellular apoptosis; PCR primer; ss.	
XX		
OS	Synthetic.	
OS	Home sapiens	
XX		
PN	W09919513-A2	
XX		
PD	22-APR-1999.	
XX		
PF	09-OCT-1998; 98WC-US21315.	
XX		
PR	10-OCT-1997; 97US-0061572.	
XX		
PA	(LXRP-) LXR BIOTECHNOLOGY INC.	
XX		
PI	Erikson J, Goddard JG, Kiefer M;	
XX		
DR	WPI, 1999-277658/23.	
XX		
XX	Identification of (ant)agonists of LPA receptor EDG-2 for, e.g.	
PT	treating LPA signalling mediated diseases such as cellular apoptosis	
XX		

Human orphan G pro
Primer 90K-1 used
Factor IX mutageni
Factor IX mutageni
Mitochondrial prot
5' primer for epid
Human osteo antivi
Human extracellula
Tobacco mosaic vir
Mouse REXANK PCR p
PCR primer P3M13-
Human cystatin C 9
Human neuropilin m
Human cystatin C 9
Antisense 16FRP-5
PCR primer used to
Human FasL, Fas 11
Antisense primer f
Oligonucleotide 82
c-mpl receptor ago
Primer 82-5' for c
Mutagenic primer #
PCR primer #3 used
5' PCR primer used
ubiquitin conjugat
Primer used for am
Human ubiquitin co
5' PCR primer used
Primer for amplify